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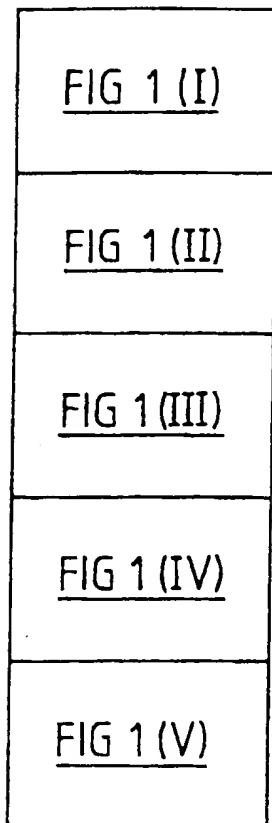


FIG 1

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FIGURE 1 (I)

AAC	AAG	AAG	GTG	ACC	AAC	CTG	TTC	TGC	TGT	AAG	TGC	CCC	50
Lys	Arg	Lys	Val	Thr	Asn	Leu	Phe	Cys	Phe	Glu	His	Cys	Pro
10						15						5	
GTC	TGC	GAG	CAC	TGC	CTG	GTA	GCC	AAT	CAC	GCC	AAG	TGC	95
Val	Cys	Glu	His	Cys	Leu	Val	Ala	Asn	His	Ala	Lys	Cys	
25						30					35		
CAG	TCC	TAC	TCT	CAA	TGG	CTC	CAA	GAT	GAC	TAC	AAC	CCC	140
Gln	Ser	Tyr	Leu	Gln	Trp	Leu	Gln	Asp	Ser	Asp	Tyr	Asn	
40						45					50		
TGC	CGC	CTG	TGC	AAC	ATA	CCC	CTG	GCC	AGC	CGA	GAG	ACG	230
Cys	Arg	Leu	Cys	Asn	Ile	Pro	Leu	Ala	Ser	Arg	Glu	Thr	
55						60					65		
C'TT	GTC	TGC	TAT	GAT	CTC	TTT	CAC	TGG	GCC	TGC	C'TC	AAT	275
Leu	Val	Cys	Tyr	Asp	Leu	Phe	His	Trp	Ala	Cys	Leu	Asn	
70						75					80		

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FIGURE 1 (II)

GCT	GCC	CAG	CTA	CCC	CGA	AAC	ACG	GCA	CCT	GCC	GGC	TAT	CAG	TGG	320
Ala	Ala	Gln	Leu	Pro	Arg	Asn	Thr	Ala	Pro	Ala	Gly	Tyr	Gln	Cys	
85												95			
CCC	AGC	TGC	AAT	GGC	CCC	ATC	TTC	CCC	CCA	ACC	AAC	CTG	GCT	GGC	365
Pro	Ser	Cys	Asn	Gly	Pro	Ile	Phe	Pro	Pro	Thr	Asn	Leu	Ala	Gly	
		100										110			
CCC	GTG	GCC	TCC	GCA	CTG	AGA	GAG	AAG	CTG	GCC	ACA	GTC	AAC	TGG	410
Pro	Val	Ala	Ser	Ala	Leu	Arg	Glu	Lys	Leu	Ala	Thr	Val	Asn	Trp	
		115						120				125			
GCC	CGG	GCA	GGA	CTG	GGC	CTC	CCT	CTG	ATC	GAT	GAG	GTG	GTG	AGC	455
Ala	Arg	Ala	Gly	Leu	Gly	Leu	Pro	Leu	Ile	Asp	Glu	Val	Val	Ser	
		130						135				140			
CCA	GAG	CCC	GAG	CCC	CTC	AAC	ACG	TCT	TTC	TCT	GAC	TGG	TCT	500	
Pro	Glu	Pro	Glu	Pro	Leu	Asn	Thr	Ser	Asp	Phe	Ser	Asp	Trp	Ser	
		145					150					155			
AGT	TTT	AAT	GCC	AGC	AGT	ACC	CCT	GGA	CCA	GAG	GAG	GTA	GAC	AGC	545
Ser	Phe	Asn	Ala	Ser	Ser	Thr	Pro	Gly	Pro	Glu	Glu	Val	Asp	Ser	
		160						165				170			

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FIGURE 1 (III)

GCC	TCT	GCT	GCC	CCA	GCC	TTC	TAC	AGC	CGA	GCC	CCC	CGG	CCC	CCA	590
Ala	Ser	Ala	Ala	Pro	Ala	Phe	Tyr	Ser	Arg	Ala	Pro	Arg	Pro	Pro	
175						180						185			
GCT	TCC	CCA	GGC	CGG	CCC	GAG	CAG	CAC	ACA	GTG	ATC	CAC	ATG	GGC	635
Ala	Ser	Pro	Gly	Arg	Pro	Glu	Gln	His	Thr	Val	Ile	His	Met	Gly	
190						195						200			
AAT	CCT	GAG	CCC	TTG	ACT	CAC	GCC	CCT	AGG	AAG	GTG	TAT	GAT	ACG	680
Asn	Pro	Glu	Pro	Leu	Thr	His	Ala	Pro	Arg	Lys	Val	Tyr	Asp	Thr	
205						210						215			
CGG	GAT	GAT	GAC	CGG	ACA	CCA	GGC	CTC	CAT	GGA	GAC	TGT	GAC	GAT	725
Arg	Asp	Asp	Asp	Arg	Thr	Pro	Gly	Leu	His	Gly	Asp	Cys	Asp	Asp	
220						225						230			
GAC	AAG	TAC	CGA	CGT	CGG	CCG	TTC	GGT	TGG	CTG	GCC	CGG	CTG	770	
Asp	Lys	Tyr	Arg	Arg	Arg	Pro	Ala	Leu	Gly	Trp	Leu	Ala	Arg	Leu	
235						240						245			
CTA	AGG	AGG	CGG	GCT	GGG	TCT	CGG	AAG	CGG	CCG	CTG	ACC	CTG	CTC	815
Leu	Arg	Ser	Arg	Ala	Gly	Ser	Arg	Lys	Arg	Pro	Leu	Thr	Leu	Leu	
250						255						260			

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FIGURE 1 (IV)

CAG	CGG	GGG	CTG	CTG	CTA	CTC	TTG	GGG	CTG	GGG	TTC	CTG	860
Gln	Arg	Ala	Gly	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Phe	Leu	
													275
GGC	CTC	CTT	GCC	CTC	ATG	TCT	CGC	CTA	GGC	GCC	GCA	GCT	905
Ala	Leu	Leu	Ala	Leu	Met	Ser	Arg	Leu	Gly	Arg	Ala	Ala	
													290
AGC	GAT	CCC	AAC	CTG	GAC	CCA	CTC	ATG	AAC	CAC	ATC	CGC	950
Ser	Asp	Pro	Asn	Leu	Asp	Pro	Leu	Met	Asn	Pro	His	Ile	
													305
GGC	CCC	TCC	TGA	GGCCCCCTTGCG	TTCGGGCTAG	GGCAGGCCCTAG	GATGTGGGTT	1002					
Cly	Pro	Ser	*										
CTGTGGAGGA	GAGGGGGGT	AATGGGGAGG	CTGAGGGCAC	CTCTTCAC	TG	1052							
CCCCCTCTCCC	TCAAGGCCAA	GACACTAAGA	CCCCAGACCC	AAAGCCAAAGT		1102							
CCACCAAGT	GGCTCGGCAGG	CCAGGCCCTGG	AGTCCCCGTTG	GCTCAAGCAT		1152							

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FIGURE 1 (v)
TTGTCTTGAC TTGCTTCTC CCGGGTCTCC AGGCCTCCGAC CCCCTGGCCCC
ATGAAGGAGC TGGCAGGTGG AAATAAACAA CAACTTTATT
1202
1242

Figure 2

35| AA155210 AA155210 mr98e01.r1 Stratagene mouse embryonic carcinoma
1#9373171 Mus musculus cDNA clone 505496 5
Query: : MGLCXC PKRKVNLFCFTEHRVNVCEHCLVANHAKCIVQSYLQWLNQDSDDYNPCRLTNIPL 65
: MGLCXC PKRKVNLFCFTEHRVNVCEHCLVANHAKCIVQSYLQWLNQDSDDYNPCRLCN PL
Subject: 38 MGLCXC PKRKVNLFCFTEHRVNVCEHCLVANHAKCIVQSYLQWLNQDSDDYNPCRLCNPL 27

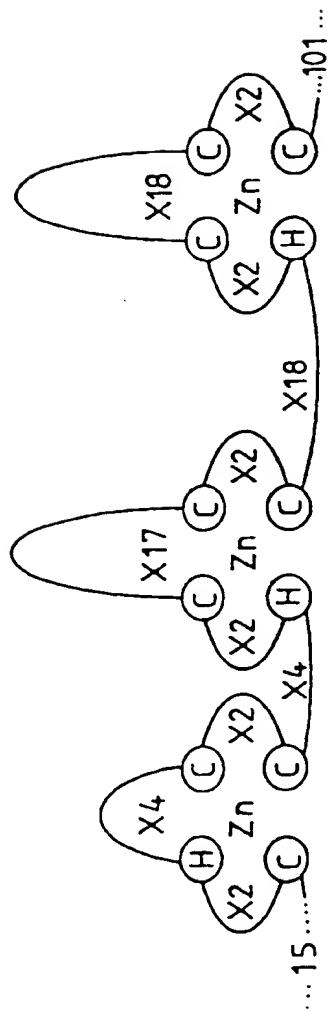
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FIGURE 3

dbj|D75913 | CELK11G3F C. elegans cDNA clone ykl11g3:5' end, single read.

Query:	7	PKRKVTNLFCFEHRVNVCEHCLVANHAKCIVQSYLQOWLQDSDDYNPNCRLCNIPLASRETT	66			
		PKRKVTNLF + EHRVNVCE LV NH C+VQSYL WL D DY+PNC LC L +T				
Subject:	1	PKRKVTNLFXYEHRVNVCEXLVDNHPNCVVQSYLTWLTQDYDPNCSSLCKTTLXEGDTI	180			
Query:	67	RLVCYDLFWACLNERAAGLPRNTAPAGYQCP	98	PSCNGPIFPPNQ	109	
		RL C L HW C +E P TAP GY+CP		P C+ +FPP+Q		
Subject:	181	RLNCLHLLHWKCFDEWXGNFPDTTAPXGYRCP	276	275	PCCSQEVFPPDQ	310

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FIG 4

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FIGURE 5

sp | P46580 | YLBS_CAEEL HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN
CHROMOSOME III gi | 500728 (U10402) C34E10.5 gene product
[Caenorhabditis elegans]

Query: 56 CNIPLASRETTRLLVCYDLFHWACLNERRAAQLPRNTAPAGYQCPSC 100
C+I L ++ + L C LF W C+ E A + + + +CP C
Sbjct: 1222 CSICLENKNPSSALFCGHILFCWTCTIQEHAVAATSSASTSSARCPQC 1266

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FIGURE 6

gi | 703468 | (L29051) homologous to GATA-binding transcription factor
 [Schizosaccharomyces pombe]

Query: 35 CIVQSYLQWLQDSDYNPNCRCLNI 58

C + +W +D NP C C +

Sbjct: 175 CATTNTPKWRRDESGNPICNACGL 198

Query: 162 SSTPGPPEEVDSASSAAPAFYSQAPRPPASPPGRPEQHTVIHMGNPEPLTHAPRKVYDTRDDD 221

+S PEE S S S P+ SP+ +Q +I P +V + D

Sbjct: 441 ASLLNPEEEPPNSSDKQPSMSNGPKSEVSPSQSQQQAPLIQSSTSPPVSLQQFPPEVQGSNVDK 500

Query: 222 RTPGLH 227

R L+

Sbjct: 501 RNYALN 506

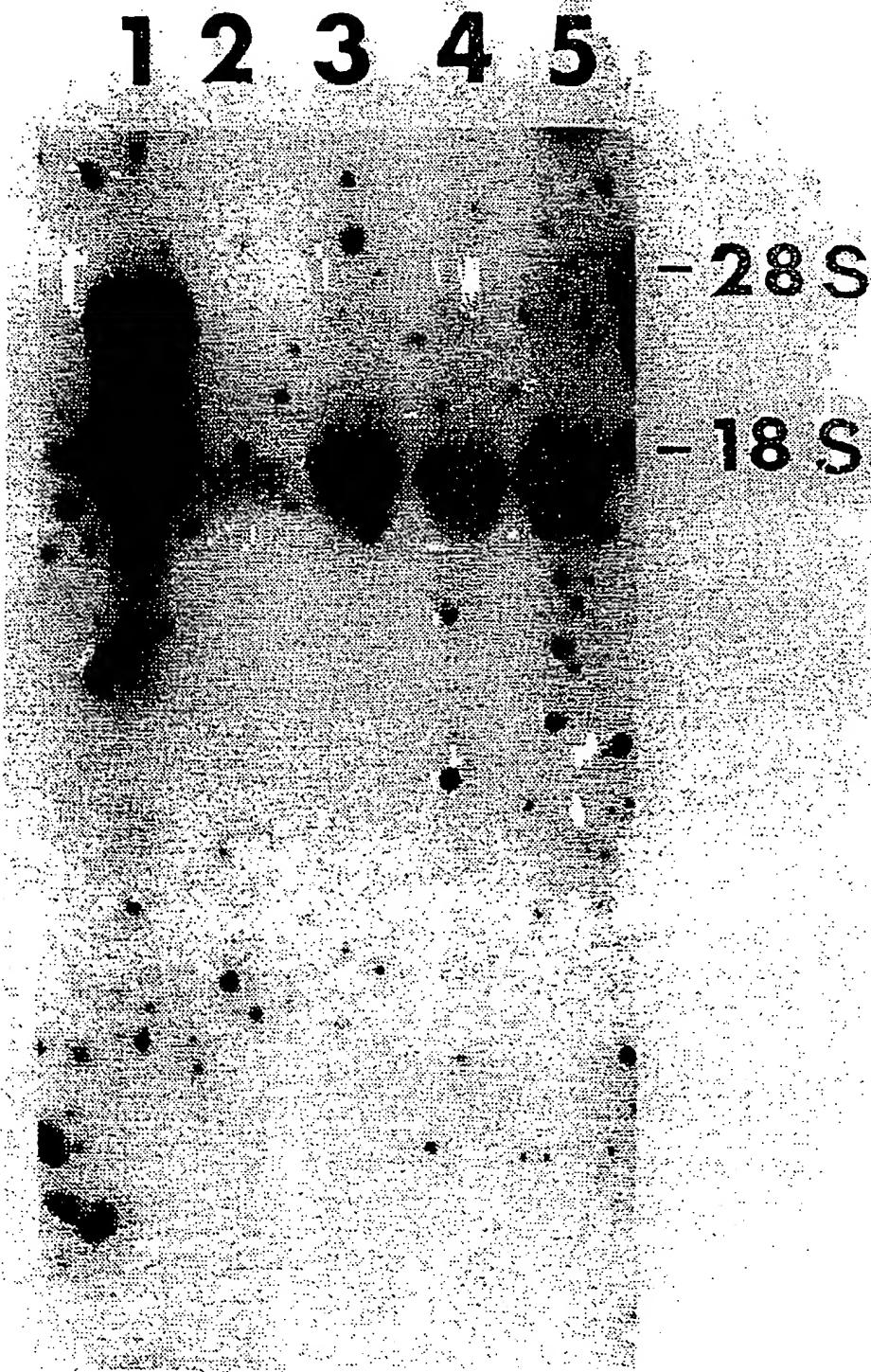
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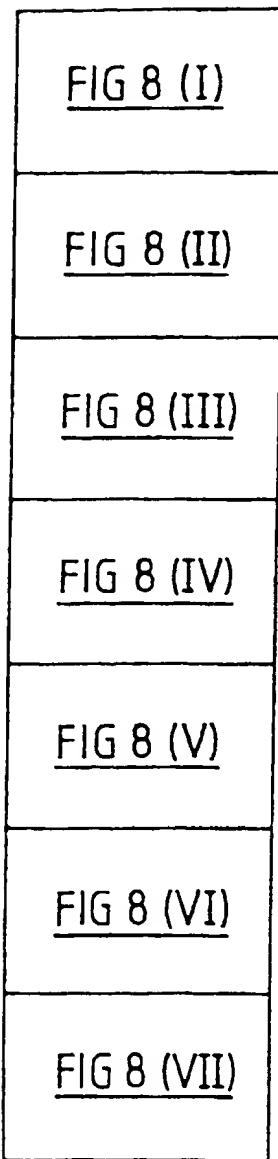
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FIG 7



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FIG 8

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FIGURE 8 (I)

gb | AA074703 | AA074703 zm76g07.rl Stratagene neuroepithelium (#937231)

Homo sapiens cDNA clone 531612 5'

Length = 417

Plus Strand HSPs:

Score = 818 (226.0 bits), Expect = 6.1e-103, Sum P(5) = 6.1e-103

Identities = 206/259 (79%), Positives = 206/259 (79%), Strand = Plus/Plus

Query: 446 GGCCTCCCTCTGATCGATGAGGTGGTGGCCAGGCCAGAGCCCTAACACGTTCTGAC 505

Subject: 49 GGGCTCCCTCTGATCGATGAGGTGATAAGCCAGGCCAGGCCCTAACATTCCCTCAGAC 108

Query: 506 TTCTCTGACTGGTCTAGTTTAATGCCAGCAGTACCCCTGGACAGGAGGTAGACAGC 565

Subject: 109 TTCTCTGATTGGTCCAGCTTAAATGCCACCCACTCTGTGCAAGAGGAGAGCCAGC 168

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FIGURE 8 (II)

Query: 566 GCCCTCTGCCAGCCTTCTACAGCCAGGCCCCAGCTTCCCCAGGCCGG 625
 Sbjct: 169 ACTCCATCTGCACCTGCTTCTATAGCCAGGCTCCCCCTCCCAAGCCGT 228

Query: 626 CCCGAGCACACAGTGATCCACATGGCAATCCCTGAGCCCTTGACTCACGCCCTAGG 685
 Sbjct: 229 CCCGAGCACACAGTCATACACATGGGAGTACTGAAGCCCTGGCACACGCCCAAGG 288

Query: 686 AAGGTGTATGATAACGGGG 704
 Sbjct: 289 AAAGTATATGACACACGGG 307

Score = 230 (63.6 bits), Expect = 6.1×10^{-3} , Sum P(5) = 6.1×10^{-3}
 Identities = 50/55 (90%), Positives = 50/55 (90%), Strand = Plus/Plus

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FIGURE 8 (III)

Query: 398 GCACCTGAGAGAGAAAGCTGGCCACAGTCAACTGGGGGGCAGGACTGGCCTTCC 452
 Sbjct: 2 GCACCTGAGAGAAAAGCTAGCCACAGTCAACTTGCCCCAGGACTGGCTCCC 56

Score = 175 (48.4 bits), Expect = 6.1e-103, sum P(5) = 6.1e-103
 Identities = 39/44 (88%), Positives = 39/44 (88%), Strand = Plus/Plus

Query: 767 GCCTTGGGTTGGCTGGCCGGCTAAGGAGCCGGCTGGTC 810
 Sbjct: 373 GCTCTGGGCTGGCTGGCCAGCTGCTCAGGAGCCGGCTGGTC 416

Score = 139 (38.4 bits), Expect = 6.1e-103, sum P(5) = 6.1e-103
 Identities = 31/35 (88%), Positives = 31/35 (88%), Strand = Plus/Plus

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FIGURE 8 (IV)

Query: 731 GGAGACTGTGACCGATGACAAGTACCGACGGTGGCC 765
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 336 GGAGACTGTGATGATGACAATAACGGCCGGCC 370

Score = 133 (36.8 bits), Expect = 6.1e-103, Sum P(5) = 5.1e-103
Identities = 29/32 (90%), Positives = 29/32 (90%), Strand = Plus/Plus

Query: 701 CGGGATGATGACCGGACACCAGGCCATGG 732
||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 305 CGGGATGATGACCGGACAGCAGGCATTATGG 336

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FIGURE 8 (V)

gb | AA134788 | AA134788 zm81g02.rl Stratagene neuroepithelium (#937231)
Homo sapiens cDNA clone 532082 5'
Length = 368

Plus Strand HSPs:

Score = 563 (155.6 bits), Expect = 3.8e-87, Sum P(3) = 3.8e-87
Identities = 147/190 (77%), Positives = 147/190 (77%), Strand = Plus/Plus

Query: 498 CGTCTGACTTCTGACTGGTCTAGTTAAATGCCAGGTACCCCTGGACCGAGGAGG 557
Sbjct: 103 CCTCAGACTTCTCTGATTGGTCCAGCTTAATGCCACCACCTCTGTGCAAGAGGAGA 162

FIGURE 8 (VI)

Query: 558 TAGACAGGGCCTCTGCTGGCCAGGCCATTACAGGCCAGGGCCCCGGCCCCAGGTTCCC 617
Sbjct: 163 GAGCCAGGCACTCCATCTGGCCTGCTTCTATAGCCAGGCTCCCGCCCTCCCTCCC 222

Query: 618 CAGGCCGGCCGAGCAGCACACAGTGATCCACATGGCAATGCCATTGACTCACG 677
Sbjct: 223 CAAGCCGTCCCGAGCAGCACACAGTCATAACATGGGAGTACTGAAGCCCTGGCACACG 282

Query: 678 CCCCTAGGAA 687
Sbjct: 283 CCCCAAGGAA 292

Score = 454 (125.4 bits), Expect = 3.8e-87, Sum P(3) = 3.8e-87

Identities = 94/98 (95%), Positives = 94/98 (95%), Strand = Plus/Plus

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FIGURE 8 (VII)

Query: 398 GCACTGAGAGAGCTGCCACAGTCACACTGGCCCCGGCAGGA
 Sbjct: 2 GCACTGAGAGACAGCTAGCCACAGTCACACTGGCCCCGGCAGGA 457
 61

Query: 458 ATCGATGAGGTGAGGCCAGAGCCGAGCCCCCTCAA 495
 Sbjct: 62 ATCGATGAGGTGATAAGCCCAGAGCCGAGCCCCCTCAA 99

Score = 219 (60.5 bits), Expect = 3.8e-87, Sum P(3) = 3.8e-87

Identities = 51/60 (85%), Positives = 51/60 (85%), Strand = Plus/Plus

Query: 702 GGGATGATGACCGGACACCGGCCTCCATGGAGACTGTGACGATGACAAGTACCGACGTC 761
 Sbjct: 309 GGATTGATGACCGGACAGCAGGCATTCATGGAGACTGTGATGACAATAACGCCGCC 368

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FIGURE 9

W32939 human

TACCGCCCTTCGGAACCAAGTGCAGCGGCCGATCAGTAACACAGACTGGGATCGATCGGGCTTGTAAAG

AA242159 mouse

CTTCGGCGCTTTCATTACCGTACGCACCGTCA-CGATCGGCATCGGGAGATCGGACTTGGCAAG

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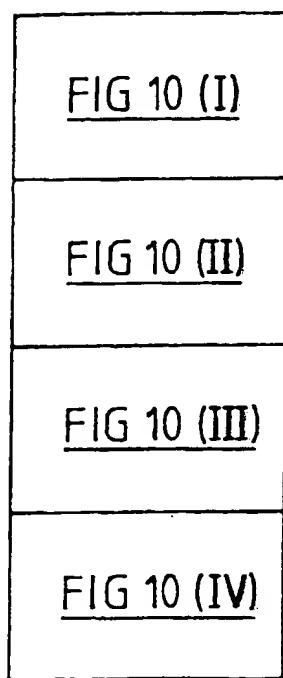
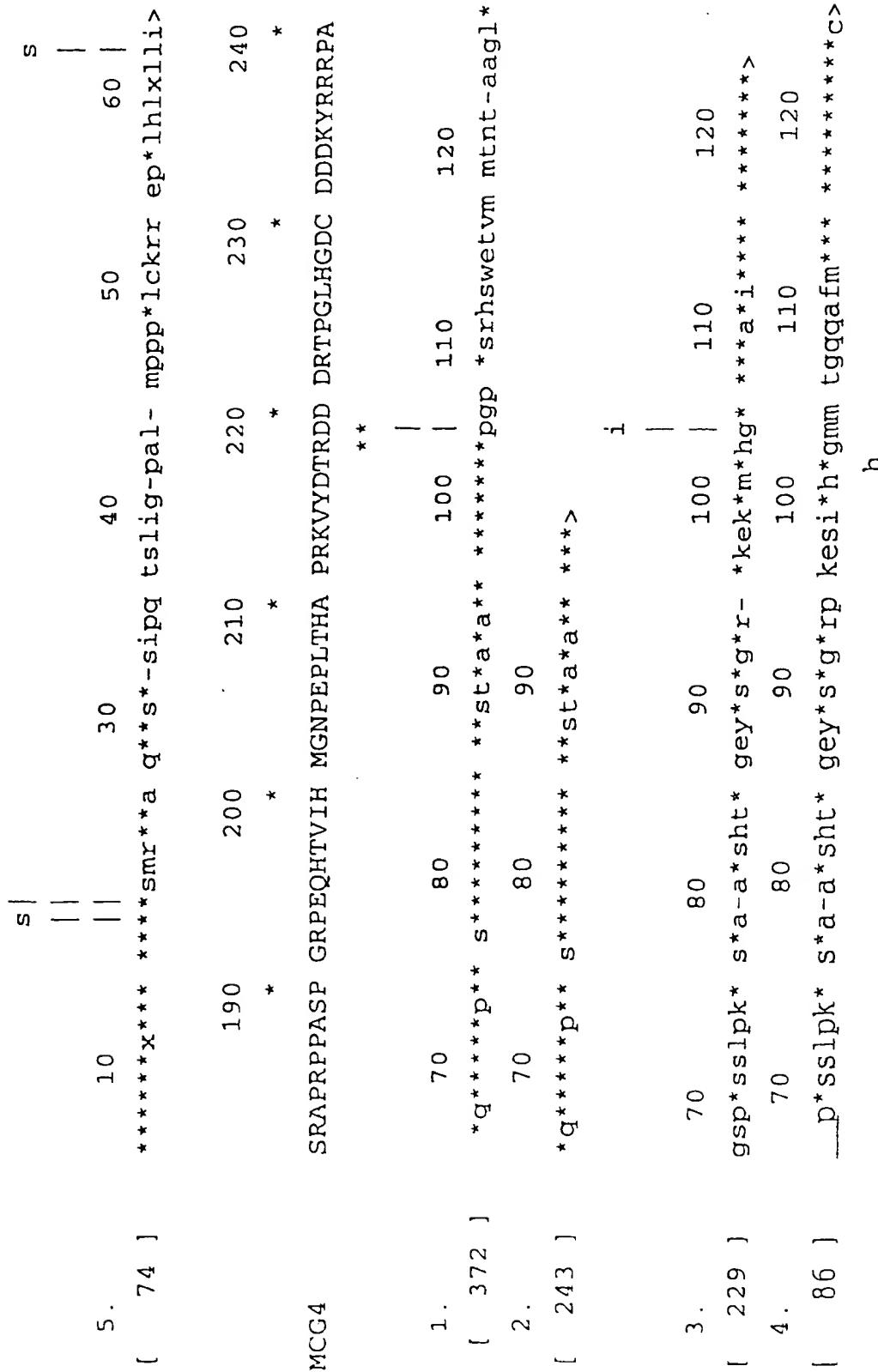


FIG 10

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FIGURE 10 (II)

Substitute Sheet (Rule 26)



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FIGURE 10 (III)

Substitute Sheet (Rule 26)

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FIGURE 10 (IV)

Search Analysis for Sequence: MCG4

Search from 1 to 310

Date: September 22, 1997

Matrix: pam250 matrix
Score Region from 1 to 310
Maximum possible score: 1598

Aligned sequences:

1. = EST AA074703 phase 1 translation
2. = EST AA134788 phase 3 translation
3. = EST AA134788 phase 2 translation
4. = EST AA074703 phase 3 translation
5. = EST AA074703 phase 2 translation
6. = EST AA134788 phase 1 translation

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FIGURE 11
Domains of MC G 4



acidic domain consensus: 9/34 negatively charged amino acids, 0/34 positively charged

basic domain consensus: 13/55 positively charged amino acids, 0/55 negatively charged

leucine zipper domain consensus: $\text{LX}_6\text{LX}_6\text{RX}_6\text{LX}_6\text{L}$

alternate "novel" leucine zipper-like motif where leucine would not be aligned along the one surface of an alpha helix domain: (aa 261)
 $\text{LX}_6\text{LX}_6\text{LX}_6\text{LX}_6\text{L}$ (aa 286)

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<u>FIG 12 (I)</u>	<u>FIG 12 (II)</u>
<u>FIG 12 (III)</u>	<u>FIG 12 (IV)</u>

FIG 12

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FIG 12 (I)
 Sequences producing High-scoring Segment Pairs:

gn1| PID| e2336178
 gi| 1293099
 gi| 1655941
 pir| s30356
 sp| P43069| CC25_CANAL
 sp| P28818| GNRP_RAT
 prf| 1814463A
 pir| B46199
 gn1| PID| e238680
 pir| s22693
 sp| P14771| SC25_YEAST
 sp| P26674| STE6_SCHPO
 pir| s28407
 sp| P27671| GNRP_MOUSE
 gi| 386047
 sp| Q02342| CC25_SACKL
 pir| s14177
 gi| 433720
 gn1| PID| e241744
 gi| 3484

(Z70752 F25B3.3 [Caenorhabditis ele...
 (U53884) aimless RasGEF [Dictyosteli...
 (U67326) Ras-GRF2 [Mus musculus]
 CDC25 protein homolog - yeast (Cand...
 CELL DIVISION CONTROL PROTEIN 25
 GUANINE NUCLEOTIDE RELEASING PROTEIN...
 guanine nucleotide-releasing factor ...
 nucleotide-exchange-factor homolog c...
 (X97560) hypothetical protein L1309...
 CDC25 protein homolog - mouse/gi 50...
 SCD25 PROTEIN /gi 457494 (M26647) SD...
 STE6 PROTEIN /pir s28098 ste6 prote...
 CDC25 protein homolog - mouse
 GUANINE NUCLEOTIDE RELEASING PROTEIN...
 (s62035) Ras-specific guanine nucleo...
 CELL DIVISION CONTROL PROTEIN 25 /pi...
 SCD25 protein - yeast (Saccharomyces...
 (L26584) CDC25 [Homo sapiens]
 (Z68880) T14G10.2 [Caenorhabditis el...
 (X03579) CDC25 protein (aa 1-1588) [...]

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High Score	smallest Sum Probability P(N)	N
307	3.0e-124	8
202	7.8e-22	5
152	3.6e-16	4
150	2.2e-15	3
150	2.2e-15	3
166	2.6e-15	3
166	2.6e-15	3
167	1.1e-14	1
158	3.0e-14	3
167	3.7e-14	2
158	4.6e-14	3
160	5.2e-14	2
167	1.2e-13	3
167	1.2e-13	3
153	2.0e-13	2
142	4.5e-13	2
152	5.7e-13	3
153	6.0e-13	3

FIG 12 (II)

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sp| P04821| CC25_YEAST CELL DIVISION CONTROL PROTEIN 25 /pi...
 gi| 915328 (U24070) Munc13-1 [Rattus norvegicus]
 pir||A46199 nucleotide-exchange-factor homolog c...
 pdb||1PTR| Molecule: Protein Kinase C Delta Ty...
 gi| 915330 (U24071) Munc13-2 [Rattus norvegicus]
 gi| 474982 (D21239) 'C3G protein' [Homo sapiens...
 gi| 1763306 (U75361) Munc13-3 [Rattus norvegicus]
 gi| 806957 guanine-nucleotide exchange factor C...
 sp| Q03385| GNDS_MOUSE GUANINE NUCLEOTIDE DISSOCIATION STIM...
 pir||BVBYL1 LTE1 protein - yeast (Saccharomyces...
 gi| 452242 (D21354) a putative guanine nucleotid...
 sp| P07866| LTE1_YEAST LOW TEMPERATURE ESSENTIAL PROTEIN /P...
 gi| 509050 (Z22521) protein kinase C delta [Hom...
 gi| 520587 (D10495) protein kinase C delta-type...
 sp| P05130| KPC1_DROME PROTEIN KINASE C, BRAIN ISOZYME (PKC...
 pir||S35704 protein kinase C (EC 2.7.1.-) delta...
 sp| Q05655| KPCD_HUMAN PROTEIN KINASE C, DELTA TYPE (NPKC-D...
 pir||S40279 protein kinase C mu - human /pir A5...
 sp| P09215| KPCD_RAT PROTEIN KINASE C, DELTA TYPE (NPKC-D...
 gi| 520878 (Z34524) serine/threonine protein ki...
 gi| 1519719 (U68142) RalGDS-like [Homo sapiens]

FIG 12 (III)

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FIG 12 IV

157	7.2e-13	1	1
136	3.4e-12	3	3
136	3.4e-12	3	3
151	5.5e-12	1	1
149	5.6e-12	1	1
136	1.5e-11	2	2
150	1.6e-11	3	3
131	3.3e-11	2	2
153	6.4e-11	1	1
128	7.8e-11	3	3
133	1.0e-10	1	1
139	1.9e-10	1	1
139	2.7e-10	1	1
139	2.7e-10	1	1
137	4.0e-10	1	1
137	4.6e-10	1	1
137	4.7e-10	1	1
137	4.7e-10	1	1
137	4.9e-10	1	1
135	9.0e-10	1	1
133	1.8e-09	1	1
115	3.8e-09	3	3

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FIG 13a (I)FIG 13a (II)FIG 13a(III)FIG 13a (IV)FIG 13a (V)FIG 13a (VI)FIG 13a(VII)FIG 13a(VIII)FIG 13a (IX)FIG 13a (X)FIG 13a

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CG	ATT	TCA	TTC	CTC	GCT	CCC	CAC	AGG	TCC	CTC	TCC	CCA	AAA	TAT	44
Ile	Ser	Phe	Leu	Ala	Pro	His	Arg	Ser	Leu	Ser	Pro	Lys	Tyr		
1															10
TCC	CAT	CTT	GTC	CTA	GCC	CAT	CCC	CCA	GAC	TAT	CTC	AAG	GAC	CAG	89
Ser	His	Leu	Val	Leu	Ala	His	Pro	Pro	Asp	Tyr	Leu	Lys	Asp	Gln	
15															25
CTG	TCC	CCA	CGC	CCC	CGA	CCT	CCA	CTA	GGC	CTG	TGC	CAC	CCG	CTG	134
Leu	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Leu	Gly	Leu	Cys	His	Pro	Leu	
30															40
CCT	GCA	GGA	AGA	CGC	CCG	GTC	CCG	GGC	GGG	GTG	AGC	CCC	ATG	GGA	179
Pro	Ala	Gly	Arg	Arg	Pro	Val	Pro	Gly	Arg	Vai	Ser	Pro	Met	Gly	
45															55
ACG	CAG	CGC	C'TG	TGT	GGC	GGC	ACT	CAA	GGC	TGG	CCT	GGC	TCA	224	
Thr	Gln	Arg	Leu	Cys	Gly	Arg	Gly	Thr	Gln	Gly	Trp	Pro	Gly	Ser	
60															70
AGT	GAA	CAG	CAC	GTC	CAG	GAG	GCG	ACC	TCG	TCC	GCG	GGT	TTG	CAT	269
Ser	Glu	Gln	His	Vai	Gln	Glu	Ala	Thr	Ser	Ser	Ala	Gly	Leu	His	
75															85

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TCT	GGG	GTG	GAC	GAG	CTG	GGG	GTT	CGG	TCC	GAG	CCC	GGT	GGG	AGG	314
Ser	Gly	Val	Asp	Glu	Leu	Gly	Val	Arg	Ser	Glu	Pro	Gly	Gly	Arg	
90										100					
CTC	CCG	GAG	CGC	AGC	CTG	GGC	CCA	GCC	CAC	CCC	GCC	CCG	GCC	GCC	359
Leu	Pro	Glu	Arg	Ser	Leu	Gly	Pro	Ala	His	Pro	Ala	Pro	Ala	Ala	
105										115					
<u>ATG</u>	GCA	GGC	ACC	CTG	GAC	CTG	GAC	AAG	GGC	TGC	ACG	GTG	GAG	GAG	404
Met	Ala	Gly	Thr	Leu	Asp	Leu	Asp	Lys	Gly	Cys	Thr	Val	Glu	Glu	
120										130					
C'TG	CTC	CCG	GGG	TGC	ATC	GAA	GCC	TTC	GAT	GAC	TCC	GGG	AAG	GTG	449
Leu	Leu	Arg	Gly	Cys	Ile	Glu	Ala	Phe	Asp	Asp	Ser	Gly	Lys	Val	
135										145					
CGG	GAC	CCG	CAG	CTG	GTG	CGC	ATG	TTC	CTC	ATG	CAC	CCC	TGG	494	
Arg	Asp	Pro	Gln	Leu	Val	Arg	Met	Phe	Leu	Met	Met	His	Pro	Trp	
150						155					160				
TAC	ATC	CCC	TCC	TCT	CAG	CTG	GCG	GCC	AAG	CTG	CTC	CAC	ATC	TAC	539
Tyr	Ile	Pro	Ser	Ser	Gln	Leu	Ala	Ala	Lys	Leu	Leu	His	Ile	Tyr	
165										170					

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CAA	CAA	TCC	CGG	AAG	GAC	AAC	TCC	AAT	TCC	CTG	CAG	GTG	AAA	ACG	584
Gln	Gln	Ser	Arg	Lys	Asp	Asn	Ser	Asn	Ser	Leu	Gln	Val	Lys	Thr	
180					185					190					
TGC	CAC	CTG	GTC	AGG	TAC	TGG	ATC	TCC	GCC	TTT	CCA	GCG	GAG	TTT	
Cys	His	Leu	Val	Arg	Tyr	Trp	Ile	Ser	Ala	Phe	Pro	Ala	Glu	Phe	629
195					200					205					
GAC	TTG	AAC	CCG	GAG	TTG	GCT	GAG	CAG	ATC	AAG	GAG	CTG	AAG	GCT	674
Asp	Leu	Asn	Pro	Glu	Leu	Ala	Glu	Gln	Ile	Lys	Glu	Leu	Lys	Ala	
210					215					220					
CTG	CTA	GAC	CAA	GAA	GGG	AAC	CGA	CGG	CAC	AGC	AGC	CTA	ATC	GAC	719
Leu	Leu	Asp	Gln	Glu	Gly	Asn	Arg	Arg	His	Ser	Ser	Leu	Ile	Asp	
225					230					235					
ATA	GAC	AGC	GTC	CCT	ACC	TAC	AAG	TGG	AAG	CGG	CAG	GTG	ACT	CAG	764
Ile	Asp	Ser	Val	Pro	Thr	Tyr	Lys	Trp	Lys	Arg	Gln	Val	Thr	Gln	
240					245					250					
CGG	AAC	CCT	GTG	GCA	CAG	AAA	AAG	CGC	AAG	ATG	TCC	CTG	TTG	TTT	809
Arg	Asn	Pro	Val	Gly	Gln	Lys	Lys	Arg	Lys	Met	Ser	Leu	Leu	Phe	
255					260					265					

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FIGURE 13 (a) (IV)

GAC	CAC	CTG	GAG	CCC	ATG	GAG	CTG	GCG	GAG	CAT	CTC	ACC	TAC	TTG	854
Asp	His	Leu	Glu	Pro	Met	Glu	Leu	Ala	Glu	His	Leu	Thr	Tyr	Leu	
270					275									280	
GAG	TAT	CGC	TCC	TTC	TGC	AAG	ATC	CTG	TTT	CAG	GAC	TAT	CAC	AGT	899
Glu	Tyr	Arg	Ser	Phe	Cys	Lys	Ile	Leu	Phe	Gln	Asp	Tyr	His	Ser	
285					290					295					
TTC	GTG	ACT	CAT	GGC	TGC	ACT	GTG	GAC	AAC	CCC	GTC	CTG	GAG	CGG	944
Phe	Val	Thr	His	Gly	Cys	Thr	Val	Asp	Asn	Pro	Val	Leu	Glu	Arg	
300					305					310					
TTC	ATC	TCC	CTC	TTC	AAC	AGC	GTC	TCA	CAG	TGG	GTG	CAG	CTC	ATG	989
Phe	Ile	Ser	Leu	Phe	Asn	Ser	Val	Ser	Gln	Trp	Val	Gln	Leu	Met	
315					320					325					
ATC	CTC	AGC	AAA	CCC	ACA	GCC	CCC	CAG	CGG	GCC	CTG	GTC	ATC	ACA	1034
Ile	Leu	Ser	Lys	Pro	Thr	Ala	Pro	Gln	Arg	Ala	Leu	Val	Ile	Thr	
330					335					340					

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FIGURE 13 (a) (V)

CAC	TTT	GTC	CAC	GTG	GCG	GAG	AAG	CTG	CTA	CAG	CTG	CAG	AAC	TTC	1079
His	Phe	Val	His	Val	Ala	Glu	Lys	Leu	Leu	Gln	Leu	Gln	Asn	Phe	
345										355					
AAC	ACG	CTG	ATG	GCA	GTC	GGG	GGC	CTG	AGC	CAC	AGC	TCC	ATC	1124	
Asn	Thr	Leu	Met	Ala	Val	Gly	Gly	Leu	Ser	His	Ser	Ser	Ile		
360										370					
TCC	CGC	CTC	AAG	GAG	ACC	CAC	AGC	CAC	GTT	AGC	CCT	GAG	ACC	ATC	1169
Ser	Arg	Leu	Lys	Glu	Glu	Thr	His	Ser	Val	Ser	Pro	Pro	Glu	Thr	
375										385					
AGG	CTC	TGG	GAG	GGT	CTC	ACG	GAA	CTA	GTG	ACG	GGG	ACA	GGC	AAC	1214
Lys	Leu	Trp	Glu	Gly	Leu	Thr	Glu	Leu	Val	Thr	Ala	Thr	Gly	Asn	
390										400					
TAT	GGC	AAC	TAC	CGG	CGT	CGG	CAC	GCA	TGT	GTG	GGC	TTC	CGC	1259	
Tyr	Gly	Asn	Tyr	Arg	Arg	Arg	Leu	Ala	Ala	Cys	Val	Gly	Phe	Arg	
405										415					
TTC	CCG	ATC	CTG	GGT	GTG	CAC	CTC	AAG	GAC	CTG	GCC	CTG	CAG	1304	
Phe	Pro	Ile	Leu	Gly	Val	His	Leu	Lys	Asp	Leu	Val	Ala	Leu	Gln	
420										430					

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CTG	GCA	CTG	CCT	GAC	TGG	CTG	GAC	CCA	GCC	CGG	ACC	CGG	CTC	AAC	1349
Leu	Ala	Leu	Pro	Asp	Trp	Leu	Asp	Pro	Ala	Arg	Thr	Arg	Leu	Asn	
435										445					
GGG	GCC	AAG	ATG	AAG	CAG	CTC	TTT	AGC	ATC	CTG	GAG	CTG	GCC	1394	
Gly	Ala	Lys	Met	Lys	Gln	Leu	Phe	Ser	Ile	Leu	Glu	Glu	Leu	Ala	
450					455					460					
ATG	GTG	ACC	AGC	CTG	CGG	CCA	CCA	GTA	CAG	GCC	AAC	CCC	GAC	CTG	1439
Met	Val	Thr	Ser	Leu	Arg	Pro	Pro	Val	Gln	Ala	Asn	Pro	Asp	Leu	
465					470					475					
CTG	AGC	CTG	CTC	ACG	GTG	TCT	CTG	GAT	CAG	TAT	ACG	GAG	GAT	1484	
Leu	Ser	Leu	Leu	Thr	Val	Ser	Leu	Asp	Gln	Tyr	Gln	Thr	Glu	Asp	
480					485					490					
GAG	CTG	TAC	CAG	CTG	TCC	CTG	CAG	CGG	GAG	CCG	CGC	TCC	AAG	TCC	1529
Glu	Leu	Tyr	Gln	Leu	Ser	Leu	Gln	Arg	Glu	Pro	Arg	Ser	Lys	Ser	
495					500					505					

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FIGURE 13 (a) (VII)

TCG	CCA	ACC	AGC	CCC	ACG	AGT	TGC	ACC	CCA	CCC	CGG	CCC	CCG	1574	
Ser	Pro	Thr	Ser	Pro	Thr	Ser	Cys	Thr	Pro	Pro	Arg	Pro	Pro		
510		515		520		525		530		535		540			
GTA	CTG	GAG	GAG	TGG	ACC	TCG	GCT	GCC	AAA	CCC	AAG	CTG	GAT	CAG	1619
Val	Leu	Glu	Glu	Trp	Trp	Ser	Ala	Ala	Lys	Pro	Lys	Leu	Asp	Gln	
525		530		535		540		545		550		555		560	
GCC	CTC	GTG	GTG	GAG	CAC	ATC	GAG	AAG	ATG	GTG	GAG	TCT	GTG	TTC	1664
Ala	Leu	Val	Val	Glu	His	Ile	Glu	Lys	Met	Val	Glut	Ser	Val	Phe	
540		545		550		555		560		565		570		575	
CGG	AAC	TTT	GAC	GTC	GAT	GGG	GAT	GGC	CAC	ATC	TCA	CAG	GAA	GAA	1709
Arg	Asn	Phe	Asp	Val	Asp	Gly	Asp	Gly	Gly	Ile	His	Ile	Ser	Gln	
555		560		565		570		575		580		585		590	
TTC	CAG	ATC	ATC	CGT	GGG	AAC	TTC	CCT	TAC	CTC	AGC	GCC	TTT	GGG	1754
Phe	Gln	Ile	Ile	Arg	Gly	Asn	Phe	Pro	Tyr	Leu	Ser	Ala	Phe	Gly	
570		575		580		585		590		595		595		595	
GAC	CTC	GAC	CAG	AAC	CAG	GAT	GGC	TGC	ATC	AGC	AGG	GAG	GAG	ATG	1799
Asp	Leu	Asp	Gln	Asn	Gln	Asp	Gly	Cys	Ile	Ser	Arg	Glu	Glu	Met	
585		590		595		595		595		595		595		595	

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FIGURE 13 (a) (VIII)

GTT	TCC	TAT	TTC	CTG	CGC	TCC	AGC	TCT	GTG	TTG	GGG	GGG	CGC	ATG	1844
Val	Ser	Tyr	Phe	Leu	Arg	Ser	Ser	Ser	Val	Leu	Gly	Gly	Arg	Met	
600				605						610					
GGC	TTC	GTA	CAC	AAC	TTC	CAG	GAG	AGC	AAC	TCC	TTG	CGC	CCC	GTC	1889
Gly	Phe	Val	His	Asn	Phe	Gln	Glu	Ser	Asn	Ser	Leu	Arg	Pro	Val	
615				620						625					
GCC	TGC	CGC	CAC	TGC	AAA	GCC	CTG	ATC	CTG	GGC	ATC	TAC	AAG	CAG	1934
Ala	Cys	Arg	His	Cys	lys	Ala	Ile	Leu	Ile	Leu	Gly	Ile	Tyr	Lys	Gln
630					635					640					
GGC	CTC	AAA	TGC	CGA	GCC	TGT	GGA	GTC	AAC	TGC	CAC	AAG	CAG	TGC	1979
Gly	Leu	Lys	Cys	Arg	Ala	Cys	Gly	Val	Asn	Cys	His	Lys	Gln	Cys	
645					650					655					
AAG	GAT	CGC	CTG	TCA	GTT	GAG	TGT	CGT	CGG	CGC	AGG	CAG	AGT	GTG	2024
Lys	Asp	Arg	Leu	Ser	Val	Glu	Cys	Arg	Arg	Arg	Ala	Gln	Ser	Val	
660					665					670					

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FIGURE 13 (a) (IX)

AGC CTG GAG GGG TCT GCA CCC TCA CCC TCA CCC ATG CAC AGC CAC 2069
 Ser Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His
 675 680 685

CAT CAC CGC GCC TTC AGC TTC TCT CTG CCC CGC CCT GGC AGG CGA 2114
 His His Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg
 690 695 700

GGC TCC AGG CCT CCA GAG ATC CGT GAG GAG GAG GTA CAG ACG GTG 2159
 Gly Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val
 705 710 715

GAG GAT GGG GTG TTT GAC ATC CAC TTG TA ATAGATGCTG 2198
 Glu Asp Gly Val Phe Asp Ile His Leu *
 720 725

TGGTTGGATC AAGGACTCAT TCCTGCCCTTG GAGAAAATACTTCAACCAAGA 2248
 CGAGGGAGCC TGGGGTGTG GGGGCAGGAG GCTGGGGATG GGGGGGGAT 2293

ATGAGGGTGG CATGCAGGCTG AGGGCAGGGC CAGGGCTGGT GTCCCTAAGG 2348

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FIGURE 13 (a) (x)
TGTACAGAC TCTTGTGAAT ATTGTATT TCCAGATGGA ATAAAAAGGC
2398
CCGTGTAATT AACCTTC (A)n
2416

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FIGURE 13 (b)

CGATTCAATT CCTCGCTCCC	CACAGGTCCC	TCTCCCCAAA	ATATTCCCAT	50
CTTGTCTTAG CCCATCCCC	AGAACTATCTC	AAGGACCAGC	TGTCCCCACG	100
CCCCCGACCT CCACTAGGCC	TGTGCCACCC	GCTGCCCTGCA	GGAAAGACGCC	150
CGGTCCCCGGG CCGGGTTAG	CCC CAT GGG AAC GGG GTT CGG TCC GAG			196
* Pro His Gly Asn Gly Val Arg Ser Glu				
				1
				5
CCC GGT GGG AGG CTC CCG GAG CGC AGC CTG GGC CCA GCC CAC				238
Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His				
10				
15				20
CCC GCG CCG GCC ATG GCA GGC ACC CTG GAC CTG GAC AAG				280
Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys				
25				
30				35
GGC TGC ACG GTG GAG GAG CT				300
Gly Cys Thr Val Glu Glu Leu				
40				

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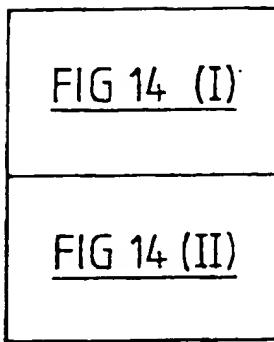


FIG 14

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FIGURE 14 (I)

1	MAGTLDLDKGCG...TVEELLRGCGIEAF...DDSGKVRDPQLVURMFLLMMHFW MSSKVEEDQHQELLTDQLVARCVCFCFDVDEEDEVEDIEFDALFLSHQW	45 50
46	YIPSSSQLAAKLLHIYQQSRKDNNSNSLQVKRTCHLVRYWISAFPAEFDLNPE LSDSLSLITHFVNFYQETRNVEQRE...AVCRAVSFWIEKFPMHFDQPO	95 97
51	LAEQIKELKALLDQEGRNRRHSSLIDIDSVPPTYKWKQRQVTQRNPVGQKK... VCAQVVVRKTIADINENIRNGL.DVSAALPSFAWLRAVSVRNPLAKQTIV	143 146
96	RKMSLIFDHLPEPMELAEHLTYLEYR	168
98	RVDFETLPTPGTPPPPPIASKKFSLTAFSLSEVQASPSDISTSLSSHIDYR	196
144	SFCKKILEQDYHSSFVTHGCTVDNPVLERFISLNFNSVSQWVQLMILSKPTAP	218
147	VLSTISITELKQYVKDGHLRSCPMLERSISVENNLSNWVQCLLNLKTPK	246
169	QRALVITHFVHYAEKLLOLONENTLMAVVGGLSHSSISRLKETHSHVSPE ERAELVKEYVHAKHLRKINNENTLMSVVGITHSSVARIAKTVAVLSND	268 296
197	TIKLWEGLTTELVTATGNYGNYRRRLAAC.VGFRFPILGVHLKDLVALQLA	317
219	TIKKELTQLTNLLSAQHNFCEYRKALGACNKFRIPPIIGVHLKDLVAINC	346
247		
269		
297		

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FIGURE 14 (II)

3 18	LPDWLDPARTRLNGAKMKQLFSSILEELAMVTSLRPPV. QANPDLSSLLTV	3 66
3 47	GANFEKT. . KCISSDKLUVKLSKLLSNFLVNQKGHNLPENNMDLINTLKV	3 94
3 67	SLDQYQTEDELYQLSLQREPRSKSSPSTSPTSCPTPPPRPPVILEEWTSAAKP	4 16
3 95	SLDIRYNDDDIYELSLREPKTFMN. . . . FEPSSRGLVFAEWASGVTV	4 37
4 17	KLDQALVVEHIEKMWESVRFNFDVDDGDDGHISQOEQQIIRGNFPYLSAFGD	4 66
4 38	APDNATVSKHISAMVDAVEKHYDHDRDGEISQOEQQLIAGNFPFIDAFVN	4 87
4 67	LDONODGCISREEMVSYFLRSS. SVLGGGRMGFVHNFOESENNSLRPVACRHC	5 15
4 88	IDVDDMDGOISKDELKTYFMAANKNTKDLRRGFKHNFHEITTELTPTTCNHC	5 37
5 16	KALILGIYKOGLKCRACGVNCHKOCKJDRLSVECRRAQSVSLEGSAPS	5 65
5 38	NKLLWGLIROGEKCKDCGGLAVHSCCKSNAVAECRRKSSSNLTRAWEWFA	5 87
5 66	PMHSHHHRAFSESLPRPGRRGSSRPPEIREEEVQTVEDGVFDIHL	6 09
5 88	PRGSMRSRIINTC. . . . NNSGSTPDEEIGLVSPLACEEVFEDDDL	6 27

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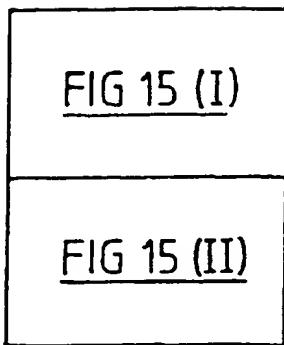


FIG 15

FIGURE 15 (I)

human	CGATTTCACT	CCTCGCTCCC	CACAGGTCCC	TCTCCCCAA	ATATTCCCCAT	CTTGTCCTAG	60
human	CCCATCCCCC	AGACTATCTC	AAGGACCAGC	TGTCCCCACG	CCCCGGACCT	CCACTAGGCC	120
human	TGTGCCACCC	GCTGCCCTGCA	GGAAGGACGCC	CGGTCCCCGG	CCGGGTAGC	CCCATGGGAA	180
human	CGCAGGCCCT	GTTGGCCGC	GGGACTCAAG	GCTGGCCTGG	CTCAAGTGA	CAGCACGTCC	240
mouse			***tca*g*	***ag***	*****	*****a*g***	>
human	AGGAGGGCAG	CTCGTCCGGCG	GGTTTGCATT	CTGGGGGTGGA	CGAGGCTGGGG	GTTCCGCTCCCG	300

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acāga

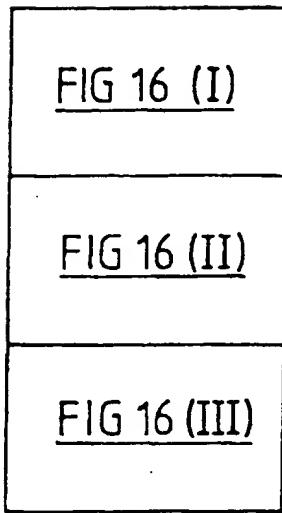
FIGURE 15 (II)

mouse * * * * * * * * * * * * t * * * * * * * * * * a * * t * * a * * * * a * * * * * * * * * * * * * * * >
 human TGATGCACCC CTGGTACATC CCCTCCTCTC AGCTGGCGGC CAAGCTGCTC CACATCTTAC 540
 mouse * * * * * * * * * * * * a * * t * * * * * * * * * * t * >
 human AACAAATCCCG GAAGGACAAAC TCCAAATTCCC TGCAGGGTCAA AACGTGCCAC CTGGTCAGGT 600
 mouse * g * >
 human ACTGGATCTC CGCCCTTCCCA GCGGAGTTTG ACTTGAACCC GGAGTTGGCT GAGCAGATCA 660
 mouse * * * * * * * * * * * * a * * * * * * * * * * * * a * >
 human AGGAGGCTGAA GGCTCTGCTA GACCAAGGAAG GGAACCGACG GCACAGCAGC CTAATCGACA 720
 mouse * >
 human TAGACACGGT
 mouse * c * * g * * t * *

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FIG 16

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FIGURE 16 (I)

CACGCCCTCGG	AAGGGAGGGT	TGGGGTCGGT	GGTTTCACAG	TGAGTGTGTC	50									
TGAAGGCCAA	TGGTCCGGAAA	CCGTTACCCG	CTCTCCTAG	GCC CGG CTA	98									
			*	Ala Arg Leu										
			1											
GTG	GGG	ACC	CCA	ACC	GCC	TGC	GGC	TCC	CCC	TCC	CAA	GTT	CCT	140
Val	Gly	Thr	Pro	Thr	Ala	Cys	Gly	Cys	Pro	Ser	Gln	Val	Pro	
														15
CCC	TGT	TGG	CCA	GGC	ATC	CAG	GTC	TCC	AGT	CTC	CGA	GCT	GCG	182
Pro	Cys	Trp	Pro	Gly	Ile	Gln	Val	Ser	Ser	Ser	Leu	Arg	Ala	
														20
GAG	AAC	CCA	CCG	CCA	CAT	GCG	GCC	CCT	TTC	CAT	TCG	ACC	224	
Glu	Asn	Pro	Pro	Pro	His	Ala	Ala	Ala	Pro	Phe	His	Ser	Thr	
														35
CTG	TGG	GGA	GCC	AGG	CTT	CCG	GGG	CCC	CGT	TCC	TGT	GTG	266	
Leu	Trp	Gly	Ala	Arg	Leu	Pro	Gly	Pro	Arg	Ser	Ser	Cys	Val	
														50
AAC	TGG	GCC	CCC	CGC	CCC	CAT	TCC	ACA	TCA	AGG	CCG	CGT	308	
Asn	Trp	Ala	Pro	Arg	Pro	His	Ser	Gln	Thr	Ser	Arg	Pro	Arg	
														65
														70

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CTC	CAG	ATA	GCC	ACG	ATT	TCA	TTC	CTC	GCT	CCC	CAC	AGG	TCC	350
Leu	Gln	Ile	Ala	Thr	Ile	Ser	Phe	Leu	Ala	Pro	His	Arg	Ser	
75														
CTC	TCC	CCA	AAA	TAT	TCC	CAT	CTT	GTC	CTA	GCC	CAT	CCC	CCA	392
Leu	Ser	Pro	Lys	Tyr	Ser	His	Leu	Val	Leu	Ala	His	Pro	Pro	
90														
GAC	TAT	CTC	AAG	GAC	CAG	CTG	TCC	CCA	CGC	CCC	CGA	CCT	CCA	434
Asp	Tyr	Leu	Lys	Asp	Gln	Leu	Ser	Pro	Arg	Pro	Arg	Pro	Pro	
CTA	GGC	CTG	TGC	CAC	CCG	CTG	CCT	GCA	GGA	AGA	CGC	CCG	GTC	476
Leu	Gly	Leu	Cys	His	Pro	Leu	Pro	Ala	Gly	Arg	Arg	Pro	Val	
CCG	GGC	CGG	GTT	AGC	CCC	ATG	GGA	ACG	CAG	CGC	CTG	TGT	GGC	518
Pro	Gly	Arg	Val	Ser	Pro	*	Pro	His	Gly	Asn				
130														

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CGC	GGG	ACT	CAA	GGC	TGG	CCT	GGC	TCA	AGT	GAA	CAG	CAC	GTC	560
Arg	Gly	Thr	Gln	Gly	Trp	Pro	Gly	Ser	Ser	Glu	Gln	His	Val	
145						150					155			
CAG	GAG	GCG	ACC	TCG	TCC	GCG	GGT	TGG	CAT	TCT	GGG	GTG	GAC	602
Gln	Glu	Gly	Ala	Thr	Ser	Ala	Gly	Leu	His	Ser	Gly	Val	Asp	
						155					160			165
GAG	CTG	GGG	GTT	CGG	TCC	GAG	CCC	GGT	GGG	AGG	CTC	CCG	GAG	644
Glu	Ileu	Gly	Val	Arg	Ser	Glu	Pro	Gly	Gly	Arg	Leu	Pro	Glu	
						170					175			180
CGC	AGC	CTG	GGC	CCA	GCC	CAC	CCC	GCG	CCG	GCG	ATG	GCA	686	
Arg	Ser	Ileu	Gly	Pro	Ala	His	Pro	Ala	Pro	Ala	Ala	Met	Ala	
						185					190			
GGC	ACC	CTG	GAC	CTG	GAC	AAG	GGC	TGC	ACG	GTG	G	720		
Gly	Thr	Ileu	Asp	Ileu	Asp	Lys	Gly	Cys	Thr	Val				
195						200					205			

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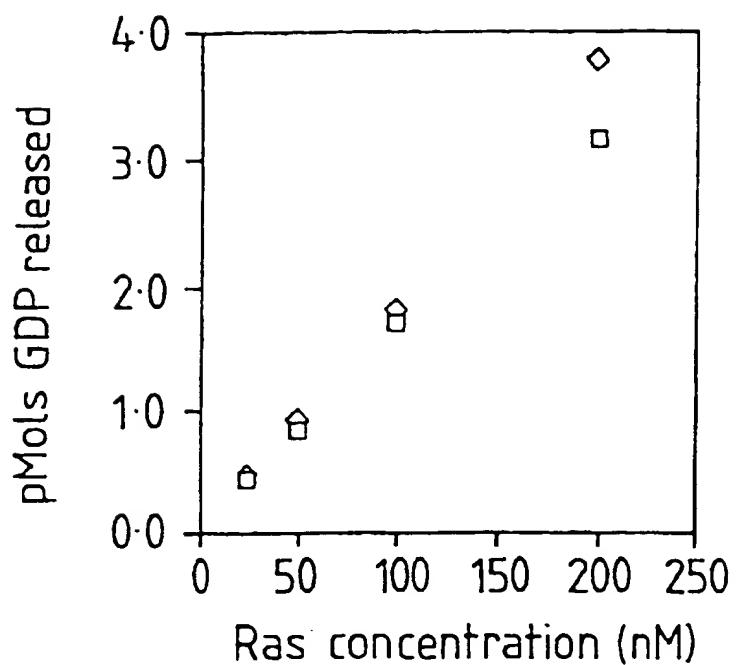
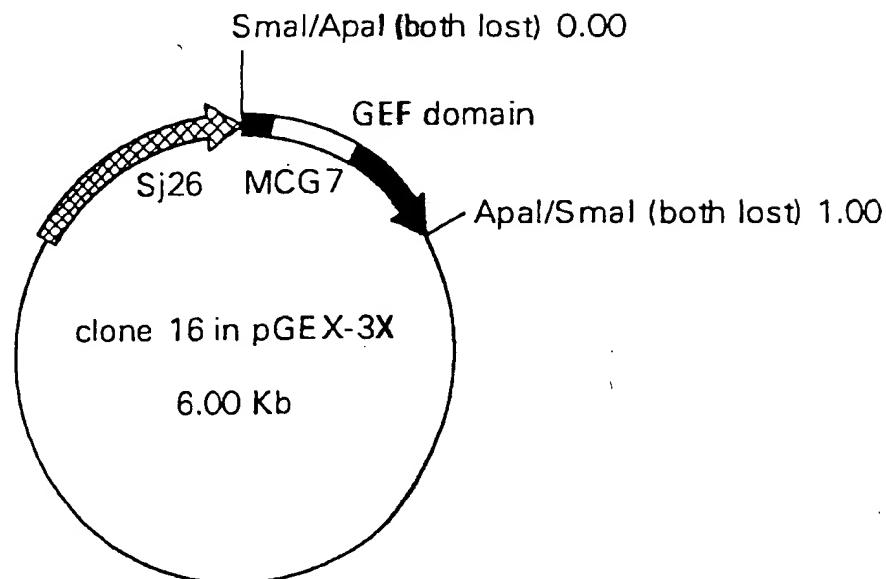
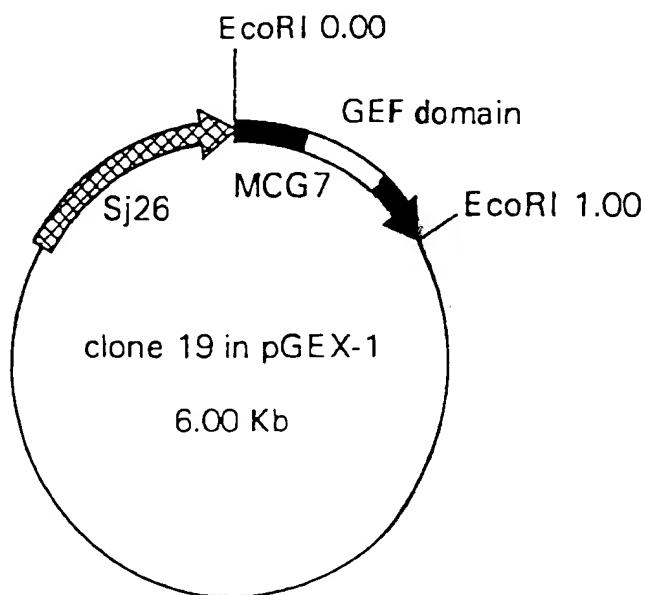


FIGURE 17

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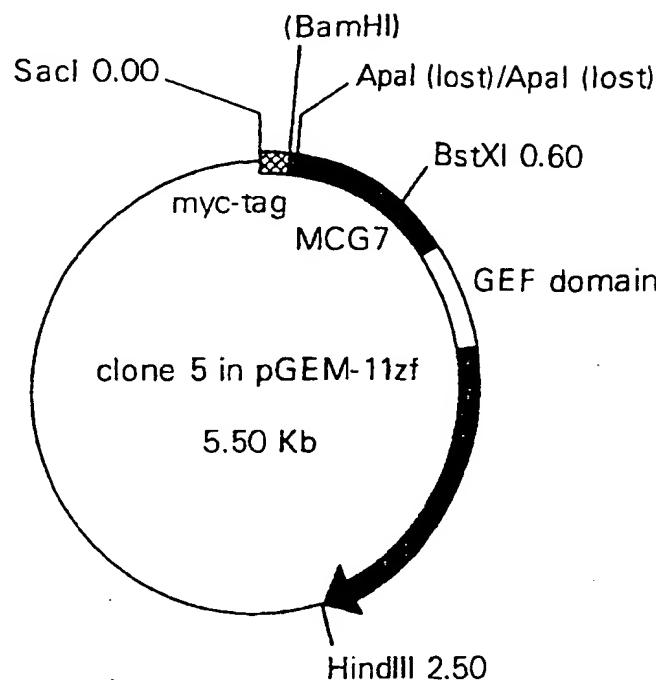
FIGURE 18 (Cont. I)

Plasmid name: clone 16 in pGEX-3X
Plasmid size: 6.00 kb

FIGURE 18 (Cont. II)

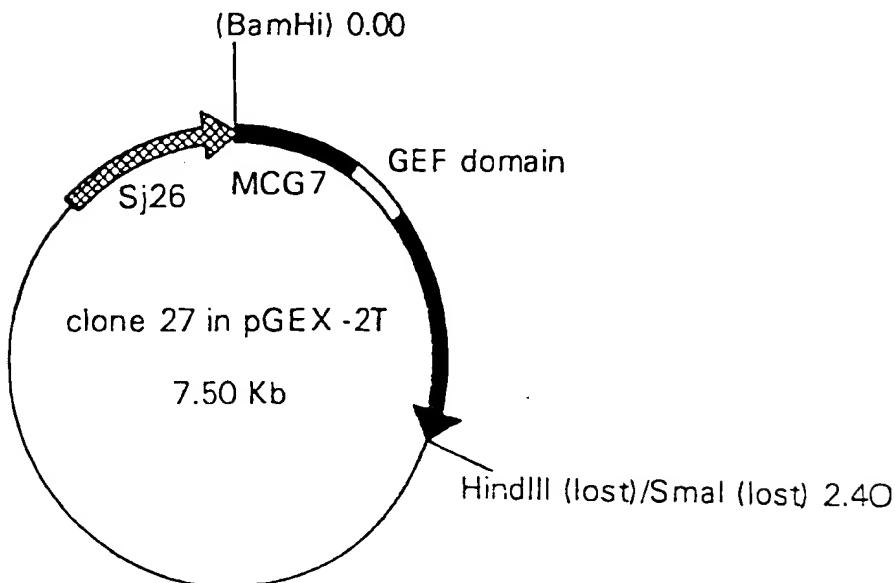
Plasmid name: clone 19 in pGEX-1
Plasmid size: 6.00 Kb

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FIGURE 18 (Cont. III)

Plasmid name: clone 5 in pGEM-11zf
Plasmid size: 5.50 kb

2000-01-01 00:00:00



Plasmid name: clone 27 in pGEX-2T
Plasmid size: 7.50 kb

FIGURE 18 (Cont. IV)

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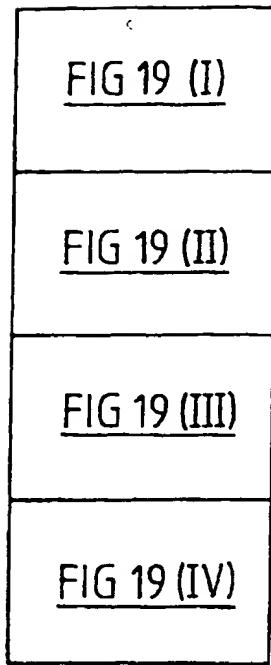


FIG 19

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FIGURE 19 (I)

ATG	CCG	CCC	TTA	CTG	CCC	CTG	CGC	CTG	TGC	CGG	43
CGCCGCCGCC	CGC	AAC	CCT	CCC	TCC	CGG	CTC	GGA	GCG	GCC	
Met	Pro	Leu	Leu	Pro	Leu	Arg	Leu	Cys	Arg		
1	5	10	15	20	25	30	35	40	45	50	55
CTG	TGG	CCC	CGG	TCC	AGA	CCC	AGT	ACT	TAT	TAT	127
Ileu	Trp	Pro	Arg	Asn	Pro	Pro	Ser	Thr	Tyr	Tyr	
15	20	25	30	35	40	45	50	55	60	65	70
GGG	GGG	CAG	CGG	TCC	AGA	CCC	AGT	ACT	TAT	GAA	169
Ala	Gly	Gln	Arg	Ser	Arg	Pro	Ser	Thr	Tyr	Glu	
30	35	40	45	50	55	60	65	70	75	80	85
GAG	GAT	CCT	GGT	GCC	AGC	AGC	GAG	GAA	GTG	AAA	211
Gly	Val	Val	His	Pro	Gly	Ala	Ser	Thr	Glu	CGA	
40	45	50	55	60	65	70	75	80	85	90	95
TTC	TCC	AAG	TCC	AAA	GAG	CTG	CAC	CCA	CGG	GAC	253
Phe	Phe	Ser	Ser	Lys	Glu	Leu	His	Pro	Asp	Arg	
55	60	65	70	75	80	85	90	95	100	105	110

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FIGURE 19 (II)

GCA	TAC	CGT	GTG	CTC	AGC	CGT	GAG	CAG	AGC	CGC	CGC	AGC	TAT	295
Ala	Tyr	Arg	Val	Leu	Ser	Arg	Glu	Gln	Ser	Arg	Arg	Ser	Tyr	95
85								90						
GAT	GAC	CAG	CTC	CGC	TCA	GGT	AGT	CCC	CCA	AAG	TCT	CCA	CGA	337
Asp	Asp	Gln	Leu	Arg	Ser	Gly	Ser	Pro	Pro	LYS	Ser	Pro	Arg	
				100					105					
ACC	ACA	GTC	CAT	GAC	AAG	TCT	GCC	CAC	CAA	ACA	CAC	AGC	TCC	379
Thr	Thr	Val	Val	His	Asp	Lys	Ser	Ala	Gln	Thr	His	Ser	Ser	
								115		120				
TGG	ACA	CCC	CCC	AAC	GCA	CAG	TAC	TGG	TCC	CAG	TTT	CAC	AGC	421
Trp	Thr	Pro	Pro	Asn	Ala	Gln	Tyr	Trp	Ser	Gln	Phe	His	Ser	
								130			135			
GTG	AGG	CCA	CAG	GGG	CCC	CAG	TTG	AGG	CAG	CAA	CAC	AAA	463	
Val	Arg	Pro	Gln	Gly	Pro	Gln	Leu	Arg	Gln	Gln	Gln	His	Lys	
								145			150			
CAA	AAC	AAA	CAA	GTG	CTG	GGG	TAC	TGC	CTC	CTC	CTC	ATG	CTG	505
Gln	Asn	Lys	Gln	Val	Leu	Gly	Tyr	Cys	Leu	Leu	Leu	Met	Leu	
			155					160				165		

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FIGURE 19 (III)						
GGG GGC ATG GGC	CTG CAC TAC ATT GCC	TTC AAG AAG GTG AAG				547
Ala Gly Met Gly	Leu His Tyr Ile Ala	Phe Arg Lys Val Lys				
170		175				
CAG ATG CAC CTT AAC TTC ATG GAT GAA AAG GAT CGG ATC ATC						589
Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile Ile						
180		185				
ACA GCC TTC TAC AAC GAA GGC CGG GCA CGG GCC AGG GCC AAC						631
Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg Ala Asn						
195		200				
AGA GGC ATC CTT CAG CAG GAG CGA CAA CGG CTA GGG CAG CGG						673
Arg Gln Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg						
210		215				
CAG CCG CCA CCA TCC GAG CCA ACC CAA GGC CCC GAG ATC GTG						715
Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val						
225		230				
CCC CGG GGC CCC TGA GGGCTC ACCTGGATGG GGCCCTGGCACT						763
Pro Arg Gly Ala Gly Pro *						
240						

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813
GGGTCCCCC TTGCTTCCT TCCCTGGACG GCCGGCTCCC CGAAACGGCC
GCAATAAGT GATTTCGGCAG 832

FIGURE 19 (IV)

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FIGURE 20

>sp|P08622|DNAJ_ECOLI DNAJ PROTEIN >pir || HECDJ heat shock protein
 dnaJ -
 Escherichia coli >gi |145769 (M12565) -heat shock protein dnaJ
 [Escherichia coli] >gi |216441 (D10483) dnaJ protein
 [Escherichia coli]

Length = 376

Score = 138 (63.7 bits), Expect = 1.2e-10, P = 1.2e-10
 Identities = 25/62 (40%), Positives = 39/62 (62%)

Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNPSLHSRFVELSEAYRVLREQSRRS94
 YYE+LGV A E++A+ + + H P D R + G+ + + F E+ E A Y V L + Q R +
 Sbjct: 6 YYELLGVSKTAAEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAA65
 Query: 95 YD 96
 YD
 Sbjct: 66 YD 67

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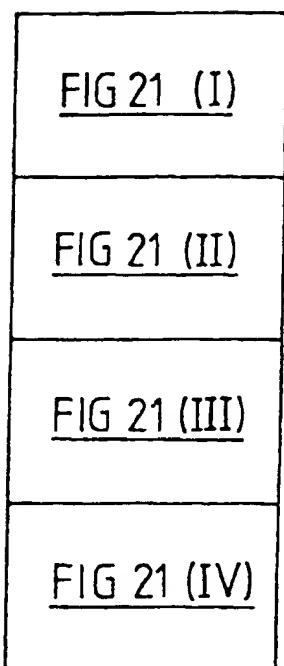


FIG 21

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FIGURE 21 (I)

>gi|1703590 (U80439) contains similarity to a DNAJ-like domain

>gi|1703590 (U80439) (Caenorhabditis elegans)

Length = 345

Score = 98 (45.2 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12

Identities = 17/37 (45%), Positives = 28/37 (75%)

Substitute Sheet (Rule 26)

Query: 28 QRSRPSTYYELLGVHPGASTEEVKRAFFSKSKELEHPD 64
+ + R T+YE+LGV A+ E+K AF++SK++HPD

Sbjct: 22 KKIRQRTTHYEVLGVESTATLSEIKSAFYAQSKKVHPD 58

Score = 74 (34.1 bits), Expect: = 5.2e-12, Sum P(3) = 5.2e-12

Identities = 17/32 (53%), Positives = 19/32 (59%)

FIGURE 21 (II)

Query: 71 SLHSRFVELSEAYRVLREQSRRRSYDDQLRSG 102
S + F+EL AY VL R RR YD QLR G
Sbjct: 64 SATASFLELKNAVDVLRRPADRRRLYQLRGG 95

Score = 39 (18.0 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12
Identities = 10/42 (23%), Positives = 19/42 (45%)

Query: 162 LLMILAGMGLHYIAFRKVKQMHNLNFMDEKDRRIITAFYNEARAR 203
L+++AG Y+ Q L+ + +D I F + R
Sbjct: 158 LVLVAGYNGGYLYLLAYMNQKQLDKLIDEDELAKCFLRQKEFR 199

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FIGURE 21 (III)

>gnl | PID | e281266 (z81030) COLG10.12 [Caenorhabditis elegans]
Length = 191
Score = 96 (44.3 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNPSLHSR 75
YYE++GV A+ +E++ AF K+K+LHPD+ + SR
Sbjct: 19 YYEIIGVSSASATRQEIRDAFLKKTKQLHPDQSSRKSSKSDSR 59

Score = 54 (24.9 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 10/22 (45%), Positives = 15/22 (68%)

Query: 75 RFVELSEAYRVLSREQSRRSYD 96
+F+ + EAY VL E+ R+ YD

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FIGURE 21 (IV)**Sbjct: 71 QFMLVKEAYDVLRNEEKRKEYD 92**

Score = 35 (16.1 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 9/44 (20%), Positives = 22/44 (50%)

Query: 141 QCPQLRQQQHKQNKQVLYCULLMLAGMGLHYIAFRKVKQMHLN 184

+ P+ + KQ ++L ++A +G + + RK++ L+

Sbjct: 145 RNPEDEYLREKQKNRMLVVLAAATVMAILLIGANIVYIRKLOQADRLS 188

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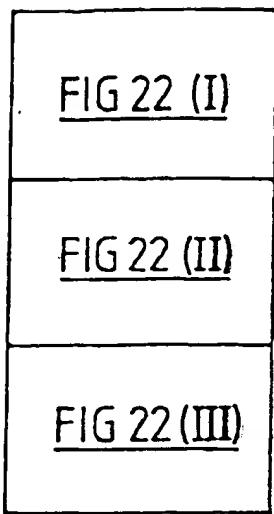


FIG 22

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FIGURE 22 (I)

```
>sp|Q10209|YAY1_SCHPO HYPOTHETICAL 44.8 KD PROTEIN C4H3.01 IN
CHROMOSOME I
>gi|1184014 (269380) unknown [Schizosaccharomyces pombe]
Length = 392
```

Score = 84 (38.8 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 13/36 (36%), Positives = 25,36 (69%)

Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNP 70
YY+LLG+ A+ ++K+A+ + + HPD+ +P +P
Sbjct: 9 YYDILLGISTDATAVDIKKAYRKILAVKYYHPDKNPDDP 44

Score = 64 (29.5 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 14/40 (35%), Positives = 23/40 (57%)

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FIGURE 22 (II)

Query: 75 RFVELSEAYRVLREQSRRSYDDQLRSGSPPKSPRTTVHD 114
+F + +SEAY+VL E+ R YD + + P+ T +D
Sbjct: 50 KFQKISEAYQVLGDEKLRSQYDQFGKEKAVPEQGFTDAYD 89

Score = 37 (17.1 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 9/29 (31%), Positives = 15/29 (51%)

Query: 190 DRIITAFYNEARARARANRGILQQERQRL 218
DR A E A+ + +++ RQR+
Sbjct: 149 DRKKNAQIRERREALAKREQEMIEDRRQRI 177

Score = 33 (15.2 bits), Expect = 0.00081, Sum P(3) = 0.00081
Identities = 8/19 (42%), Positives = 11/19 (57%)

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FIGURE 22 (III)

Query : 140 PQGPQLRQQQHKQQNQVNLG 158
PQG + Q+ + QVNLG
Sbjct : 44 PQGASEKFQKISEAYQVNLG 62

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FIGURE 23

tumorous imaginal discs [*Drosophila virilis*]

>gnl|PID|e253406 (X77635) tumorous imaginal discs [*Drosophila virilis*]
>gnl|PID|e263866 (Y07700) Tid58 protein [*Drosophila virilis*]
Length = 529

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Score = 153 (70.6 bits), Expect = 9.7e-13, P = 9.7e-13

Identities = 27/71 (38%), Positives = 44/71 (61%)

Substitute Sheet (Rule 26)

Query: 26 AGQRSPSTYYELLGVHPGASTEEVKRAFFSKSKELHPDPRPGNPSLHSRFVELSEAYRV 85
+ R + YY LGV A+ ++K+A++ +K+ HPD + +P +F ++SEAY V
Subjct: 72 SSSRMQAKDYYATLGVAKNANAKDIKKAYYELAKKYHPDTNKDDPDASKKFQDVSSEAYV 131

Query: 86 LSREQSRRSYD 96
LS +Q RR YD
Subjct: 132 LSDDQKRREYD 142

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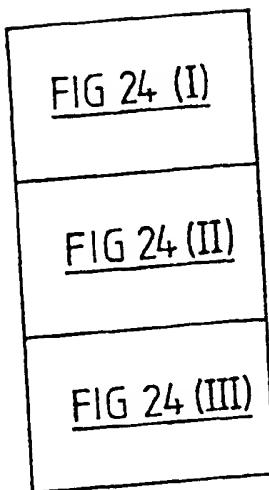


FIG 24

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FIGURE 24 (I)

FIGURE 24 (I) displays a sequence of protein fragments, each preceded by a label and followed by a sequence of amino acids. The fragments are: MCG18, HDJ-2, HDJ-1, HSJ1, MCG18, HDJ-2, HDJ-1, HSJ1, MCG18, HDJ-2, HDJ-1, HSJ1, and MCG18. The sequences are as follows:

MCG18: -MPPLPLRLCRLWP-RN--PP-----SRLLGAA
HDJ-2: MVKETTYDVLGVKPNATOQEEELKKAYRKKLALKYHDPDKN--PN---EGEKFQKQISQAYEV
HDJ-1: MGKD--YYQTGLARGASDEEIKRAYRQALRYHDPDKNKEPG---AEEKFKEIAEAYDV
HSJ1: M-AS---YYEILDVPRSASADDIIRRKAYRRKALQWHPDKN--PDNKFAEKKFKEVAEAYEV
MCG18: *.*
MCG18: AGQRSRPSTY--YELLGVH-----PGA-----ST-EEVKRAFFS-
HDJ-2: LSDAKKRELYDKGGEQALK-----EGGAGGG-----FGSPMDIFDMFFGGC
HDJ-1: LSDPRRKREIYDRYGEGLKGSGP-----SGGSGGGANGTSFSYTFHGDPHAMFAEFFFG--
HSJ1: LSDKHKREIYDRYGREGLTGTGPSRAEAGSGGP--G--FTFT-FRSPEEVFREFFFG--
*
MCG18: LSDKHKREIYDRYGREGLTGTGPSRAEAGSGGP--G--FTFT-FRSPEEVFREFFFG--
HSJ1: .
MCG18: KSKELHPDRDPGNP-----SLHSRFVELSEAYRVLREQSRRS--YDDQLRSGSPPKSPRT
HDJ-2: GRMQRERRGKNNVVIQQLSVTLEDLYNGATRKLAQKNVICDKCEGRGGKKGAVECCPNCRG
HDJ-1: GRNPFDTFFGQRNGEEGMDIDDPFSGFPMGMGGFTNVNFGRS--RSAQE PARKKQDPPVT
HSJ1: SGDPFAELFDDLGP--FSELQNRGSRHSGPFFTFSSSSFPGHSDFSSSSFSFSPGAGAFRS
Substitute Sheet (Rule 26)

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FIGURE 24 (II)

MCG1	8	TVHDKSAHOTHSSWTPPNAQY-----WSQFHSVRPQ-----GP-----QLRQQQHKQN
HDJ	2	TGMQIRIHQIGPGMVQQIQSVCMECQGHGERISPK-DRCKSCNGRKIVREKKILEVHIDK
HDJ	1	HDLRVSVSLEEYSGCTKKMK-----ISH-KRLNP---D-----GKSIRNEDKILTIEVKK
HSJ	1	VSTSTTFVQGRRITRRIME-----NGQ-ERVEVEED---GQ-----LKSVTINGVPD
	*	.
MCG1	8	KQVLGYCLL-----MLAGMGLHYIAFRKVQMHLNEMDE-KDRRIITAFYNEARARARAN
HDJ	2	GMKDGQKITFHGEQDQEPMGDIITIVLDQKDHAVFTRRGEDLFMCMIDIQLVEALCGFQ
HDJ	1	GWKEGTKITFPKEGDQTTSNNNIPADIVFVLKDKPHNIFKRDGSDVYPARISLREALCGCT
HSJ1		DLARGLELSR-RE--QQP-SVTSRSGGTQVQQTPASCPLD-SDLSEDEDLQLAMAYSLSE
	*	.
MCG1	8	RGILQQERQRLGQRQPP-PSEPTQGPEIVPRGAGP-----
HDJ	2	KPISTLDNRTIVITSHPGQIVKHGDIKCVLNEGMPIYRRPYEKGRLIIIEFKVNFPENGFL
HDJ	1	VNVPTLDGRTIPVVFK--DVIRPGMRRKVPGEGLPLPKTPEKRGDLIIIEFEVIFPER--I
HSJ1		MEAGKKPAGGREAQHR-RQGRPRPSTKIQAWGGP--RR--VRG--VKQPNAVHPQR-RR
	*	.

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FIGURE 24 (III)

MCG18	---	---
HDJ-2	SPDKLSSLLEKLLPERKEVEETDEMDQVELVDFDPNQERRHYNGEAYEDDEHHPRGGVQC	---
HDJ-1	PQTTSRTVLEQVLPI	---
HSJ1	PLAASSSEHRAQPD-----LIQILTGGSDSLWEEKRGVS-----	---
MCG18	---	---
HDJ-2	QTS	---
HDJ-1	---	---
HSJ1	---	---

* = amino acid identity in all 4 proteins
- = conservative substitution

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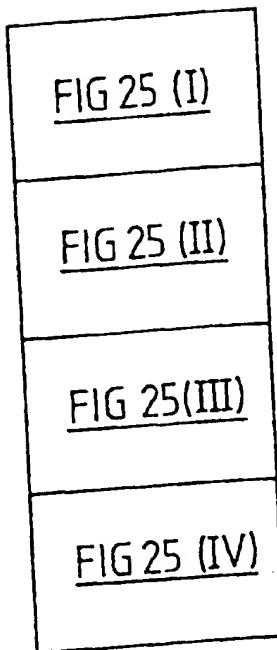


FIG 25

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FIGURE 25 (I)
CAAGGAGCCT CTGCCCTGCC GTCGTCGTC ATG CCG TCC CTG TTG CTC
Met Pro Ser Leu Leu Leu 5

TCC	ATC	CGA	CTT	CTC	ACA	GCC	ACA	GGG	CAG	CGG	—
Ser	Ile	Arg	Leu	Leu	Thr	Ala	Ala	Gln	Gly	Arg	Ser
25	30	35	40	45	50	55	60	65	70	75	80

35	AGC	GCT	GAA	GAG	ATT	AAA	CGT	GCT	TTT	TTT	ACC	AAG	TCA	AAA
Ser	Ala	Glu	Glu	Glu	Ile	Lys	Arg	Ala	Phe	Phe	Thr	Lys	Ser	Lys
							55				60			

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AGC	CGC	TTT	GTG	GAG	CTG	AAT	GAG	GCA	TAT	CGA	GTG	CTC	AGT	299
Ser	Arg	Phe	Val	Glu	Leu	Asn	Glu	Ala	Tyr	Arg	Val	Leu	Ser	
80				85									90	
CGT	GAG	GAA	AGT	CGT	CGT	AAC	TAT	GAC	CAC	CAG	CTG	CAT	TCA	
Arg	Glu	Glu	Ser	Arg	Arg	Arg	Asn	Tyr	Asp	His	Gln	Leu	His	Ser
95								100						341
GCC	AGT	CCT	CCA	AAG	TCT	TCA	GGG	AGC	ACA	GCC	GAG	CCT	AAG	
Ala	Ser	Pro	Pro	Lys	Ser	Ser	Gly	Ser	Thr	Ala	Glu	Pro	Lys	
105				110						115				383
TAT	ACG	CAA	CAG	ACA	CAC	AGC	TCC	TCC	GAA	CCC	CCC	AAC		
Tyr	Thr	Gln	Gln	Thr	His	Ser	Ser	Ser	Trp	Glu	Pro	Pro	Asn	
120					125					130				425
GCT	CAA	TAC	TGG	GCC	CAG	TTC	CAC	AGT	GTG	AGG	CCG	CAG	GGG	
Ala	Gln	Tyr	Trp	Ala	Gln	Phe	His	Ser	Val	Arg	Pro	Gln	Gly	
135									140				145	
CCG	GAG	TCA	AGG	AAG	CAG	CAG	CGT	AAA	CAC	AAC	CAG	CGG	GTC	
Pro	Glu	Ser	Arg	Lys	Gln	Gln	Arg	Lys	His	Asn	Gln	Arg	Val	
150								155					160	

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FIGURE 25 (III)	TAC	TGG	CTC	CTG	CTC	ATG	GTG	GCA	GCC	ATG	GCC	CTG
CTG	GGG	TAC	TGG	CTC	CTG	Met	Val	Ala	Gly	Met	Gly	Leu
Leu	Gly	Tyr	Cys	Leu	Leu	165	Leu	Leu	Met	170		593
CAC	TAT	GTT	GCC	TTC	AGG	AAG	CTG	GAG	CAG	GTG	CAT	CGC
His	Tyr	Val	Ala	Phe	Arg	Lys	Leu	Glu	Gln	Val	His	Arg
175												Ser
TTC	ATG	GAT	GAA	AAG	GAC	CGG	ATC	ATF	ACA	GCC	ATC	TAC
Phe	Met	Asp	Glu	Lys	Asp	Arg	Ile	Ile	Thr	Ala	Ile	Tyr
190												Asn
GAC	ACT	CGG	GCC	AGG	GCC	AAC	AGA	GCA	AGG	ATF	CAG	
Asp	Thr	Arg	Ala	Arg	Ala	Arg	Ala	Asn	Arg	Ala	Ile	Gln
205												215
CAG	GAG	CGC	CAC	GAG	AGG	CAG	CCT	CGG	GCA	GAA	CCC	TCC
Gln	Glu	Arg	His	Glu	Arg	Gln	Gln	Pro	Arg	Ala	Glu	Pro
220												Ser
												230
												719

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FIGURE 25 (IV)
 CCT CCA GAA AGC TCC AGG ATC ATG CCC CAG GAC ACA AGC
 Pro Pro Glu Ser Ser Arg Ile Met Pro Gln Asp Thr Ser
 Leu Pro 235 240
 -ATGCTCTCC CTGCTGCG

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TCCAGAACTA CACGTGCAAT AAACTCATT TCAG (A)n
 CCCCTGAGA
 *
 Pro 245

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FIGURE 26

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FIGURE 27

TTGA	AGT	CTA	GCC	CCA	TCC	TGG	TCC	AAT	GCG	CTC	TTC	GTA	
*	Ser	Leu	Ala	Pro	Ser	Trp	Ser	Asn	Ala	Leu	Leu	Val	
1													
GCC	TCC	TTT	CCC	AGC	TGC	CCG	CCC	GCC	GCC	ATG	CCG	CCC	TTA
Ala	Ser	Phe	Pro	Ser	Cys	Pro	Pro	Ala	Ala	Met	Pro	Pro	Leu
15													
CTG	CCC	CTG	CGC	CTG	TGC	CGG	CTG	TGG	CCC	CGC	AAC	CC	120
Leu	Pro	Leu	Arg	Leu	Cys	Arg	Leu	Trp	Pro	Arg	Asn	Pro	
30													
35													

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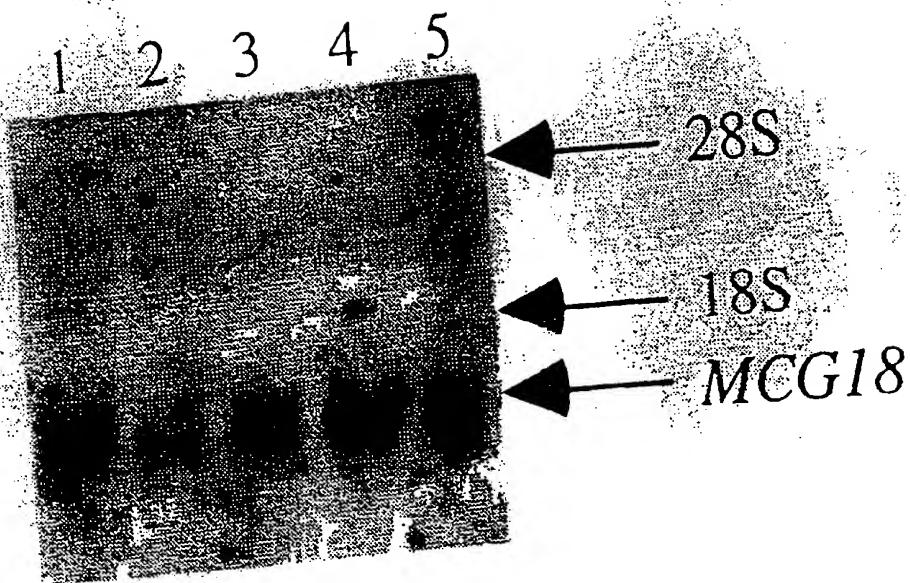


FIG 28

SUBSTITUTE SHEET (RULE 26)